SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: WILLIAMS, Lewis T.
                  ESCOBEDO, Jaime A.

  (ii) TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS

 (iii) NUMBER OF SEQUENCES: 14

  (iv) CORRESPONDENCE ADDRESS:
       (A) ADDRESSEE: Townsend and Townsend and Crew
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       (C) CITY: San Francisco
       (D) STATE: California
       (E) COUNTRY: USA
       (F) ZIP: 94105

   (v) COMPUTER READABLE FORM:
       (A) MEDIUM TYPE: Floppy disk
       (B) COMPUTER: IBM PC compatible
       (C) OPERATING SYSTEM: PC-DOS/MS-DOS
       (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

  (vi) CURRENT APPLICATION DATA:
       (A) APPLICATION NUMBER: US 08/461,917
       (B) FILING DATE: 05-JUN-1995
       (C) CLASSIFICATION:

 (vii) PRIOR APPLICATION DATA:
       (A) APPLICATION NUMBER: US 07/309,322
       (B) FILING DATE: 10-FEB-1989

 (vii) PRIOR APPLICATION DATA:
       (A) APPLICATION NUMBER: US 07/151,414
       (B) FILING DATE: 02-FEB-1988

(viii) ATTORNEY/AGENT INFORMATION:
       (A) NAME: Dow, Karen B.
       (B) REGISTRATION NUMBER: 29,684
       (C) REFERENCE/DOCKET NUMBER: 2307K-267-2-4

  (ix) TELECOMMUNICATION INFORMATION:
       (A) TELEPHONE: 415/326-2400
       (B) TELEFAX: 415/326-2422

(2) INFORMATION FOR SEQ ID NO:1:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 6373 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: cDNA

  (ix) FEATURE:
       (A) NAME/KEY: CDS
       (B) LOCATION: 129..3398

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TTGGAGCTAC AGGGAGAGAA ACAGAGGAGG AGACTGCAAG AGATCATTGG AGGCCGTGGG      60

CACGCTCTTT ACTCCATGTG TGGGACATTC ATTGCGGAAT AACATCGGAG GAGAAGTTTC     120

CCAGAGCT ATG GGG ACT TCC CAT CCG GCG TTC CTG GTC TTA GGC TGT CTT     170
          Met Gly Thr Ser His Pro Ala Phe Leu Val Leu Gly Cys Leu
          1                   5                   10

CTC ACA GGG CTG AGC CTA ATC CTC TGC CAG CTT TCA TTA CCC TCT ATC      218
Leu Thr Gly Leu Ser Leu Ile Leu Cys Gln Leu Ser Leu Pro Ser Ile
15                  20                  25                  30

CTT CCA AAT GAA AAT GAA AAG GTT GTG CAG CTG AAT TCA TCC TTT TCT      266
Leu Pro Asn Glu Asn Glu Lys Val Val Gln Leu Asn Ser Ser Phe Ser
            35                  40                  45

CTG AGA TGC TTT GGG GAG AGT GAA GTG AGC TGG CAG TAC CCC ATG TCT      314
Leu Arg Cys Phe Gly Glu Ser Glu Val Ser Trp Gln Tyr Pro Met Ser
            50                  55                  60

GAA GAA GAG AGC TCC GAT GTG GAA ATC AGA AAT GAA GAA AAC AAC AGC      362
Glu Glu Glu Ser Ser Asp Val Glu Ile Arg Asn Glu Glu Asn Asn Ser
            65                  70                  75

GGC CTT TTT GTG ACG GTC TTG GAA GTG AGC AGT GCC TCG GCG GCC CAC      410
Gly Leu Phe Val Thr Val Leu Glu Val Ser Ser Ala Ser Ala Ala His
        80                  85                  90

ACA GGG TTG TAC ACT TGC TAT TAC AAC CAC ACT CAG ACA GAA GAG AAT      458
Thr Gly Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr Glu Glu Asn
95                  100                 105                 110

GAG CTT GAA GGC AGG CAC ATT TAC ATC TAT GTG CCA GAC CCA GAT GTA      506
Glu Leu Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp Pro Asp Val
            115                 120                 125

GCC TTT GTA CCT CTA GGA ATG ACG GAT TAT TTA GTC ATC GTG GAG GAT      554
Ala Phe Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile Val Glu Asp
            130                 135                 140

GAT GAT TCT GCC ATT ATA CCT TGT CGC ACA ACT GAT CCC GAG ACT CCT      602
Asp Asp Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro Glu Thr Pro
            145                 150                 155

GTA ACC TTA CAC AAC AGT GAG GGG GTG GTA CCT GCC TCC TAC GAC AGC      650
Val Thr Leu His Asn Ser Glu Gly Val Val Pro Ala Ser Tyr Asp Ser
            160                 165                 170

AGA CAG GGC TTT AAT GGG ACC TTC ACT GTA GGG CCC TAT ATC TGT GAG      698
Arg Gln Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr Ile Cys Glu
175                 180                 185                 190

GCC ACC GTC AAA GGA AAG AAG TTC CAG ACC ATC CCA TTT AAT GTT TAT      746
Ala Thr Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe Asn Val Tyr
            195                 200                 205

GCT TTA AAA GCA ACA TCA GAG CTG GAT CTA GAA ATG GAA GCT CTT AAA      794 -
Ala Leu Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu Lys
            210                 215                 220

ACC GTG TAT AAG TCA GGG GAA ACG ATT GTG GTC ACC TGT GCT GTT TTT      842
Thr Val Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe
            225                 230                 235

AAC AAT GAG GTG GTT GAC CTT CAA TGG ACT TAC CCT GGA GAA GTG AAA      890
Asn Asn Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys
            240                 245                 250
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GGC AAA GGC ATC ACA ATG CTG GAA GAA ATC AAA GTC CCA TCC ATC AAA          938
Gly Lys Gly Ile Thr Met Leu Glu Glu Ile Lys Val Pro Ser Ile Lys
255             260             265             270

TTG GTG TAC ACT TTG ACG GTC CCC GAG GCC ACG GTG AAA GAC AGT GGA          986
Leu Val Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys Asp Ser Gly
            275             280             285

GAT TAC GAA TGT GCT GCC CGC CAG GCT ACC AGG GAG GTC AAA GAA ATG         1034
Asp Tyr Glu Cys Ala Ala Arg Gln Ala Thr Arg Glu Val Lys Glu Met
        290             295             300

AAG AAA GTC ACT ATT TCT GTC CAT GAG AAA GGT TTC ATT GAA ATC AAA         1082
Lys Lys Val Thr Ile Ser Val His Glu Lys Gly Phe Ile Glu Ile Lys
        305             310             315

CCC ACC TTC AGC CAG TTG GAA GCT GTC AAC CTG CAT GAA GTC AAA CAT         1130
Pro Thr Phe Ser Gln Leu Glu Ala Val Asn Leu His Glu Val Lys His
        320             325             330

TTT GTT GTA GAG GTG CGG GCC TAC CCA CCT CCC AGG ATA TCC TGG CTG         1178
Phe Val Val Glu Val Arg Ala Tyr Pro Pro Pro Arg Ile Ser Trp Leu
335             340             345             350

AAA AAC AAT CTG ACT CTG ATT GAA AAT CTC ACT GAG ATC ACC ACT GAT         1226
Lys Asn Asn Leu Thr Leu Ile Glu Asn Leu Thr Glu Ile Thr Thr Asp
            355             360             365

GTG GAA AAG ATT CAG GAA ATA AGG TAT CGA AGC AAA TTA AAG CTG ATC         1274
Val Glu Lys Ile Gln Glu Ile Arg Tyr Arg Ser Lys Leu Lys Leu Ile
            370             375             380

CGT GCT AAG GAA GAA GAC AGT GGC CAT TAT ACT ATT GTA GCT CAA AAT         1322
Arg Ala Lys Glu Glu Asp Ser Gly His Tyr Thr Ile Val Ala Gln Asn
            385             390             395

GAA GAT GCT GTG AAG AGC TAT ACT TTT GAA CTG TTA ACT CAA GTT CCT         1370
Glu Asp Ala Val Lys Ser Tyr Thr Phe Glu Leu Leu Thr Gln Val Pro
        400             405             410

TCA TCC ATT CTG GAC TTG GTC GAT GAT CAC CAT GGC TCA ACT GGG GGA         1418
Ser Ser Ile Leu Asp Leu Val Asp Asp His His Gly Ser Thr Gly Gly
415             420             425             430

CAG ACG GTG AGG TGC ACA GCT GAA GGC ACG CCG CTT CCT GAT ATT GAG         1466
Gln Thr Val Arg Cys Thr Ala Glu Gly Thr Pro Leu Pro Asp Ile Glu
            435             440             445

TGG ATG ATA TGC AAA GAT ATT AAG AAA TGT AAT AAT GAA ACT TCC TGG         1514
Trp Met Ile Cys Lys Asp Ile Lys Lys Cys Asn Asn Glu Thr Ser Trp
            450             455             460

ACT ATT TTG GCC AAC AAT GTC TCA AAC ATC ATC ACG GAG ATC CAC TCC         1562
Thr Ile Leu Ala Asn Asn Val Ser Asn Ile Ile Thr Glu Ile His Ser
            465             470             475

CGA GAC AGG AGT ACC GTG GAG GGC CGT GTG ACT TTC GCC AAA GTG GAG         1610
Arg Asp Arg Ser Thr Val Glu Gly Arg Val Thr Phe Ala Lys Val Glu
            480             485             490

GAG ACC ATC GCC GTG CGA TGC CTG GCT AAG AAT CTC CTT GGA GCT GAG         1658
Glu Thr Ile Ala Val Arg Cys Leu Ala Lys Asn Leu Leu Gly Ala Glu
495             500             505             510

AAC CGA GAG CTG AAG CTG GTG GCT CCC ACC CTG CGT TCT GAA CTC ACG         1706
Asn Arg Glu Leu Lys Leu Val Ala Pro Thr Leu Arg Ser Glu Leu Thr
            515             520             525
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GTG GCT GCT GCA GTC CTG GTG CTG TTG GTG ATT GTG ATC ATC TCA CTT       1754
Val Ala Ala Ala Val Leu Val Leu Leu Val Ile Val Ile Ile Ser Leu
            530                 535                 540

ATT GTC CTG GTT GTC ATT TGG AAA CAG AAA CCG AGG TAT GAA ATT CGC       1802
Ile Val Leu Val Val Ile Trp Lys Gln Lys Pro Arg Tyr Glu Ile Arg
        545                 550                 555

TGG AGG GTC ATT GAA TCA ATC AGC CCA GAT GGA CAT GAA TAT ATT TAT       1850
Trp Arg Val Ile Glu Ser Ile Ser Pro Asp Gly His Glu Tyr Ile Tyr
        560                 565                 570

GTG GAC CCG ATG CAG CTG CCT TAT GAC TCA AGA TGG GAG TTT CCA AGA       1898
Val Asp Pro Met Gln Leu Pro Tyr Asp Ser Arg Trp Glu Phe Pro Arg
575             580                 585                 590

GAT GGA CTA GTG CTT GGT CGG GTC TTG GGG TCT GGA GCG TTT GGG AAG       1946
Asp Gly Leu Val Leu Gly Arg Val Leu Gly Ser Gly Ala Phe Gly Lys
                595                 600                 605

GTG GTT GAA GGA ACA GCC TAT GGA TTA AGC CGG TCC CAA CCT GTC ATG       1994
Val Val Glu Gly Thr Ala Tyr Gly Leu Ser Arg Ser Gln Pro Val Met
            610                 615                 620

AAA GTT GCA GTG AAG ATG CTA AAA CCC ACG GCC AGA TCC AGT GAA AAA       2042
Lys Val Ala Val Lys Met Leu Lys Pro Thr Ala Arg Ser Ser Glu Lys
            625                 630                 635

CAA GCT CTC ATG TCT GAA CTG AAG ATA ATG ACT CAC CTG GGG CCA CAT       2090
Gln Ala Leu Met Ser Glu Leu Lys Ile Met Thr His Leu Gly Pro His
        640                 645                 650

TTG AAC ATT GTA AAC TTG CTG GGA GCC TGC ACC AAG TCA GGC CCC ATT       2138
Leu Asn Ile Val Asn Leu Leu Gly Ala Cys Thr Lys Ser Gly Pro Ile
655                 660                 665                 670

TAC ATC ATC ACA GAG TAT TGC TTC TAT GGA GAT TTG GTC AAC TAT TTG       2186
Tyr Ile Ile Thr Glu Tyr Cys Phe Tyr Gly Asp Leu Val Asn Tyr Leu
                675                 680                 685

CAT AAG AAT AGG GAT AGC TTC CTG AGC CAC CAC CCA GAG AAG CCA AAG       2234
His Lys Asn Arg Asp Ser Phe Leu Ser His His Pro Glu Lys Pro Lys
                690                 695                 700

AAA GAG CTG GAT ATC TTT GGA TTG AAC CCT GCT GAT GAA AGC ACA CGG       2282
Lys Glu Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp Glu Ser Thr Arg
            705                 710                 715

AGC TAT GTT ATT TTA TCT TTT GAA AAC AAT GGT GAC TAC ATG GAC ATG       2330
Ser Tyr Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr Met Asp Met
        720                 725                 730

AAG CAG GCT GAT ACT ACA CAG TAT GTC CCC ATG CTA GAA AGG AAA GAG       2378
Lys Gln Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu Arg Lys Glu
735             740                 745                 750

GTT TCT AAA TAT TCC GAC ATC CAG AGA TCA CTC TAT GAT CGT CCA GCC       2426
Val Ser Lys Tyr Ser Asp Ile Gln Arg Ser Leu Tyr Asp Arg Pro Ala
                755                 760                 765

TCA TAT AAG AAG AAA TCT ATG TTA GAC TCA GAA GTC AAA AAC CTC CTT       2474
Ser Tyr Lys Lys Lys Ser Met Leu Asp Ser Glu Val Lys Asn Leu Leu
            770                 775                 780

TCA GAT GAT AAC TCA GAA GGC CTT ACT TTA TTG GAT TTG TTG AGC TTC       2522
Ser Asp Asp Asn Ser Glu Gly Leu Thr Leu Leu Asp Leu Leu Ser Phe
            785                 790                 795
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ACC TAT CAA GTT GCC CGA GGA ATG GAG TTT TTG GCT TCA AAA AAT TGT        2570
Thr Tyr Gln Val Ala Arg Gly Met Glu Phe L u Ala Ser Lys Asn Cys
    800                 805                 810

GTC CAC CGT GAT CTG GCT GCT CGC AAC GTT CTC CTG GCA CAA GGA AAA        2618
Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala Gln Gly Lys
815                 820                 825                 830

ATT GTG AAG ATC TGT GAC TTT GGC CTG GCC AGA GAC ATC ATG CAT GAT        2666
Ile Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Met His Asp
                835                 840                 845

TCG AAC TAT GTG TCG AAA GGC AGT ACC TTT CTG CCC GTG AAG TGG ATG        2714
Ser Asn Tyr Val Ser Lys Gly Ser Thr Phe Leu Pro Val Lys Trp Met
            850                 855                 860

GCT CCT GAG AGC ATC TTT GAC AAC CTC TAC ACC ACA CTG AGT GAT GTC        2762
Ala Pro Glu Ser Ile Phe Asp Asn Leu Tyr Thr Thr Leu Ser Asp Val
        865                 870                 875

TGG TCT TAT GGC ATT CTG CTC TGG GAG ATC TTT TCC CTT GGT GGC ACC        2810
Trp Ser Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Thr
    880                 885                 890

CCT TAC CCC GGC ATG ATG GTG GAT TCT ACT TTC TAC AAT AAG ATC AAG        2858
Pro Tyr Pro Gly Met Met Val Asp Ser Thr Phe Tyr Asn Lys Ile Lys
895                 900                 905                 910

AGT GGG TAC CGG ATG GCC AAG CCT GAC CAC GCT ACC AGT GAA GTC TAC        2906
Ser Gly Tyr Arg Met Ala Lys Pro Asp His Ala Thr Ser Glu Val Tyr
                915                 920                 925

GAG ATC ATG GTG AAA TGC TGG AAC AGT GAG CCG GAG AAG AGA CCC TCC        2954
Glu Ile Met Val Lys Cys Trp Asn Ser Glu Pro Glu Lys Arg Pro Ser
                930                 935                 940

TTT TAC CAC CTG AGT GAG ATT GTG GAG AAT CTG CTG CCT GGA CAA TAT        3002
Phe Tyr His Leu Ser Glu Ile Val Glu Asn Leu Leu Pro Gly Gln Tyr
            945                 950                 955

AAA AAG AGT TAT GAA AAA ATT CAC CTG GAC TTC CTG AAG AGT GAC CAT        3050
Lys Lys Ser Tyr Glu Lys Ile His Leu Asp Phe Leu Lys Ser Asp His
    960                 965                 970

CCT GCT GTG GCA CGC ATG CGT GTG GAC TCA GAC AAT GCA TAC ATT GGT        3098
Pro Ala Val Ala Arg Met Arg Val Asp Ser Asp Asn Ala Tyr Ile Gly
975                 980                 985                 990

GTC ACC TAC AAA AAC GAG GAA GAC AAG CTG AAG GAC TGG GAG GGT GGT        3146
Val Thr Tyr Lys Asn Glu Glu Asp Lys Leu Lys Asp Trp Glu Gly Gly
                995                 1000                1005

CTG GAT GAG CAG AGA CTG AGC GCT GAC AGT GGC TAC ATC ATT CCT CTG        3194
Leu Asp Glu Gln Arg Leu Ser Ala Asp Ser Gly Tyr Ile Ile Pro Leu
                1010                1015                1020

CCT GAC ATT GAC CCT GTC CCT GAG GAG GAG GAC CTG GGC AAG AGG AAC        3242
Pro Asp Ile Asp Pro Val Pro Glu Glu Glu Asp Leu Gly Lys Arg Asn
            1025                1030                1035

AGA CAC AGC TCG CAG ACC TCT GAA GAG AGT GCC ATT GAG ACG GGT TCC        3290
Arg His Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser
    1040                1045                1050

AGC AGT TCC ACC TTC ATC AAG AGA GAG GAC GAG ACC ATT GAA GAC ATC        3338
Ser Ser Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile
1055                1060                1065                1070
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GAC ATG ATG GAC GAC ATC GGC ATA GAC TCT TCA GAC CTG GTG GAA GAC          3386
Asp Met Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp
            1075                    1080                1085

AGC TTC CTG TAA CTGGCGGATT CGAGGGGTTC CTTCCACTTC TGGGGCCACC              3438
Ser Phe Leu  *
            1090
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TCTGGATCCC GTTCAGAAAA CCACTTTATT GCAATGCGGA GGTTGAGAGG AGGACTTGGT        3498

TGATGTTTAA AGAGAAGTTC CCAGCCAAGG GCCTCGGGGA GCCTTTCTAA ATATGAATGA        3558

ATGGGATATT TTGAAATGAA CTTTGTCAGT GTTGCCTCTT GCAATGCCTC AGTAGCATCT        3618

CAGTGGTGTG TGAAGTTTGG AGATAGATGG ATAAGGGAAT AATAGGCCAC AGAAGGTGAA        3678

CTTTCTGCTT CAAGGACATT GGTGAGAGTC CAACAGACAC AATTTATACT GCGACAGAAC        3738

TTCAGCATTG TAATTATGTA AATAACTCTA ACCACGGCTG TGTTTAGATT GTATTAACTA        3798

TCTTCTTTGG ACTTCTGAAG AGACCACTCA ATCCATCCAT GTACTTCCCT CTTGAAACCT        3858

GATGTCAGCT GCTGTTGAAC TTTTTAAAGA AGTGCATGAA AAACCATTTT TGACCTTAAA        3918

AGGTACTGGT ACTATAGCAT TTTGCTATCT TTTTTAGTGT TAAAGAGATA AAGAATAATA        3978

ATTAACCAAC CTTGTTTAAT AGATTTGGGT CATTTAGAAG CCTGACAACT CATTTTCATA        4038

TTGTAATCTA TGTTTATAAT ACTACTACTG TTATCAGTAA TGCTAAATGT GTAATAATGT        4098

AACATGATTT CCCTCCACAC AAAGCACAAT TTAAAAACAA TCCTTACTAA GTAGGTGATG        4158

AGTTTGACAG TTTTTGACAT TTATATTAAA TAACATGTTT CTCTATAAAG TATGGTAATA        4218

GCTTAGTGA ATTAAATTTA GTTGAGCATA GAGAACAAAG TAAAAGTAGT GTTGTCCAGG         4278

AAGTCAGAAT TTTTAACTGT ACTGAATAGG TTCCCCAATC CATCGTATTA AAAAACAATT        4338

AACTGCCCTC TGAAATAATG GGATTAGAAA CAAACAAAAC TCTTAAGTCC TAAAAGTTCT        4398

CAATGTAGAG GCATAAACCT GTGCTGAACA TAACTTCTCA TGTATATTAC CCAATGGAAA        4458

ATATAATGAT CAGCGCAAAA GACTGGATTT GCAGAAGTTT TTTTTTTTTT TCTTCTTGCC        4518

TGATGAAAGC TTTGGCGACC CCAATATATG TATTTTTTGA ATCTATGAAC CTGAAAAGGG        4578

TCACAAAGGA TGCCCAGACA TCAGCCTCCT TCTTTCACCC CTTACCCCAA AGAGAAAGAG        4638

TTTGAAACTC GAGACCATAA AGATATTCTT TAGTGGAGGC TGGAAGTGCA TTAGCCTGAT        4698

CCTCAGTTCT CAAATGTGTG TGGCAGCCAG GTAGACTAGT ACCTGGGTTT CCATCCTTGA        4758

GATTCTGAAG TATGAAGTCT GAGGGAAACC AGAGTCTGTA TTTTTCTAAA CTCCCTGGCT        4818

GTTCTGATCG GCCAGGTTTC GGAAACACTG ACTTAGGTTT CAGGAAGTTG CCATGGGAAA        4878

CAAATAATTT GAACTTTGGA ACAGGGTTCT TAAGTTGGTG CGTCCTTCGG ATGATAAATT        4938

TAGGAACCGA AGTCCAATCA CTGTAAATTA CGGTAGATCG ATCGTTAACG CTGGAATTAA        4998

ATTGAAAGGT CAGAATCGAC TCCGACTCTT TCGATTTCAA ACCAAAACTG TCCAAAAGGT        5058

TTTCATTTCT ACGATGAAGG GTGACATACC CCCTCTAACT TGAAAGGGGC AGAGGGCAGA        5118

AGAGCGGAGG GTGAGGTATG GGGCGGTTCC TTTCCGTACA TGTTTTTAAT ACGTTAAGTC        5178

ACAAGGTTCA GAGACACATT GGTCGAGTCA CAAAACCACC TTTTTTGTAA AATTCAAAAT        5238
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GACTATTAAA CTCCAATCTA CCCTCCTACT TAACAGTGTA GATAGGTGTG ACAGTTTGTC      5298

CAACCACACC CAAGTAACCG TAAGAAACGT TATGACGAAT TAACGACTAT GGTATACTTA      5358

CTTTGTACCC GACACTAATG ACGTTAGTGA CACGATAGCC GTCTACTACG AAACCTTCTA      5418

CGTCTTCGTT ATTATTTCAT GAACTGATGG ATGACCACAT TAGAGTTACG TTCGGGGTTG      5478

AAAGAATAGG TTGAAAAAGT ATCATTCACG CTTCTGACTC GGTCTAACCG GTTAATTTTT      5538

CTTTTGGACT GATCCAAGAC ATCTCGGTTA ATCTGAACTT TATGCAAACA CAAAGATCTT      5598

AGTGTCGAGT TCGTAAGACA AATAGCGAGT GAGAGGGAAC ATGTCGGAAT AAAACAACCA      5658

CGAAACGTAA AACTATAACG ACACTCGGAA CGTACTGTAG TACTCCGGCC TACTTTGAAG      5718

AGTCAGGTCG TCAAAGGTCA GGATTGTTTA CGAGGGTGGA CTTAAACATA TACTGACGTA      5778

AACACCCACA CACACACAAA AGTCGTTTAA GGTCTAAACA AAGGAAAACC GGAGGACGTT      5838

TCAGAGGTCT TCTTTTAAAC GGTTAGAAAG GATGAAAGAT AAAAATACTA CTGTTAGTTT      5898

CGGCCGGACT CTTTGTGATA AACACTGAAA AATTTGCTAA TCACTACAGG AATTTTACAC      5958

CAGACGGTTA GACATGTTTT ACCAGGATAA AAACACTTCT CCCTGTATTC TATTTTACTA      6018

CAATATGTAG TTATACATAT ATACATAAAG ATATATCTGA ACCTCTTATG ACGGTTTTGT      6078

AAATACTGTT CGACATAGTG ACGGAAGCAA ATATAAAAAA ATTGACACTA TTAGGGGTGT      6138

CCGTGTAATT GACAACGTGA AAACTTACAG GTTTTAAATA TAAAATCTTT ATTATTTTTC      6198

TTTCTATGAA TGTACAAGGG TTTTGTTACC ACACCACTTA CACACTCTTT TTGATTGAAC      6258

TATCCCAGAT GGTTATGTTT TACATAATGC TTACGGGGAC AAGTACAAAA ACAAAATTTT      6318

GCACATTTAC TTCTAGAAAT ATAAAGTTAT TTACTATATA TTAAATTTCC TTAAG           6373
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(2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1090 amino acids
           (B) TYPE: amino acid
           (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Gly Thr Ser His Pro Ala Phe Leu Val Leu Gly Cys Leu Leu Thr
 1               5                  10                  15

Gly Leu Ser Leu Ile Leu Cys Gln Leu Ser Leu Pro Ser Ile Leu Pro
                20                  25                  30

Asn Glu Asn Glu Lys Val Val Gln Leu Asn Ser Ser Phe Ser Leu Arg
                35                  40                  45

Cys Phe Gly Glu Ser Glu Val Ser Trp Gln Tyr Pro Met Ser Glu Glu
        50                  55                  60

Glu Ser Ser Asp Val Glu Ile Arg Asn Glu Glu Asn Asn Ser Gly Leu
65                  70                  75                  80

Phe Val Thr Val Leu Glu Val Ser Ser Ala Ser Ala Ala His Thr Gly
                85                  90                  95
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Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr Glu Glu Asn Glu Leu
          100   105   110

Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp Pro Asp Val Ala Phe
          115   120   125

Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile Val Glu Asp Asp Asp
    130   135   140

Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro Glu Thr Pro Val Thr
145   150   155   160

Leu His Asn Ser Glu Gly Val Val Pro Ala Ser Tyr Asp Ser Arg Gln
              165   170   175

Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr Ile Cys Glu Ala Thr
              180   185   190

Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe Asn Val Tyr Ala Leu
          195   200   205

Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu Lys Thr Val
    210   215   220

Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe Asn Asn
225   230   235   240

Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys Gly Lys
              245   250   255

Gly Ile Thr Met Leu Glu Glu Ile Lys Val Pro Ser Ile Lys Leu Val
              260   265   270

Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys Asp Ser Gly Asp Tyr
          275   280   285

Glu Cys Ala Ala Arg Gln Ala Thr Arg Glu Val Lys Glu Met Lys Lys
    290   295   300

Val Thr Ile Ser Val His Glu Lys Gly Phe Ile Glu Ile Lys Pro Thr
305   310   315   320

Phe Ser Gln Leu Glu Ala Val Asn Leu His Glu Val Lys His Phe Val
              325   330   335

Val Glu Val Arg Ala Tyr Pro Pro Pro Arg Ile Ser Trp Leu Lys Asn
          340   345   350

Asn Leu Thr Leu Ile Glu Asn Leu Thr Glu Ile Thr Thr Asp Val Glu
          355   360   365

Lys Ile Gln Glu Ile Arg Tyr Arg Ser Lys Leu Lys Leu Ile Arg Ala
    370   375   380

Lys Glu Glu Asp Ser Gly His Tyr Thr Ile Val Ala Gln Asn Glu Asp
385   390   395   400

Ala Val Lys Ser Tyr Thr Phe Glu Leu Leu Thr Gln Val Pro Ser Ser
              405   410   415

Ile Leu Asp Leu Val Asp Asp His His Gly Ser Thr Gly Gly Gln Thr
              420   425   430

Val Arg Cys Thr Ala Glu Gly Thr Pro Leu Pro Asp Ile Glu Trp Met
          435   440   445

Ile Cys Lys Asp Ile Lys Lys Cys Asn Asn Glu Thr Ser Trp Thr Ile
    450   455   460

Leu Ala Asn Asn Val Ser Asn Ile Ile Thr Glu Ile His Ser Arg Asp
465   470   475   480

Arg Ser Thr Val Glu Gly Arg Val Thr Phe Ala Lys Val Glu Glu Thr
            485   490   495

Ile Ala Val Arg Cys Leu Ala Lys Asn Leu Leu Gly Ala Glu Asn Arg
            500   505   510

Glu Leu Lys Leu Val Ala Pro Thr Leu Arg Ser Glu Leu Thr Val Ala
        515   520   525

Ala Ala Val Leu Val Leu Leu Val Ile Val Ile Ile Ser Leu Ile Val
    530   535   540

Leu Val Val Ile Trp Lys Gln Lys Pro Arg Tyr Glu Ile Arg Trp Arg
545   550   555   560

Val Ile Glu Ser Ile Ser Pro Asp Gly His Glu Tyr Ile Tyr Val Asp
            565   570   575

Pro Met Gln Leu Pro Tyr Asp Ser Arg Trp Glu Phe Pro Arg Asp Gly
        580   585   590

Leu Val Leu Gly Arg Val Leu Gly Ser Gly Ala Phe Gly Lys Val Val
        595   600   605

Glu Gly Thr Ala Tyr Gly Leu Ser Arg Ser Gln Pro Val Met Lys Val
    610   615   620

Ala Val Lys Met Leu Lys Pro Thr Ala Arg Ser Ser Glu Lys Gln Ala
625   630   635   640

Leu Met Ser Glu Leu Lys Ile Met Thr His Leu Gly Pro His Leu Asn
        645   650   655

Ile Val Asn Leu Leu Gly Ala Cys Thr Lys Ser Gly Pro Ile Tyr Ile
        660   665   670

Ile Thr Glu Tyr Cys Phe Tyr Gly Asp Leu Val Asn Tyr Leu His Lys
        675   680   685

Asn Arg Asp Ser Phe Leu Ser His His Pro Glu Lys Pro Lys Lys Glu
    690   695   700

Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp Glu Ser Thr Arg Ser Tyr
705   710   715   720

Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr Met Asp Met Lys Gln
            725   730   735

Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu Arg Lys Glu Val Ser
            740   745   750

Lys Tyr Ser Asp Ile Gln Arg Ser Leu Tyr Asp Arg Pro Ala Ser Tyr
        755   760   765

Lys Lys Lys Ser Met Leu Asp Ser Glu Val Lys Asn Leu Leu Ser Asp
    770   775   780

Asp Asn Ser Glu Gly Leu Thr Leu L u Asp Leu Leu Ser Phe Thr Tyr
785   790   795   800

Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Lys Asn Cys Val His
                805   810   815

Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala Gln Gly Lys Ile Val
            820   825   830

Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Met His Asp Ser Asn
            835   840   845

Tyr Val Ser Lys Gly Ser Thr Phe Leu Pro Val Lys Trp Met Ala Pro
    850   855   860

Glu Ser Ile Phe Asp Asn Leu Tyr Thr Thr Leu Ser Asp Val Trp Ser
865   870   875   880

Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Thr Pro Tyr
            885   890   895

Pro Gly Met Met Val Asp Ser Thr Phe Tyr Asn Lys Ile Lys Ser Gly
            900   905   910

Tyr Arg Met Ala Lys Pro Asp His Ala Thr Ser Glu Val Tyr Glu Ile
        915   920   925

Met Val Lys Cys Trp Asn Ser Glu Pro Glu Lys Arg Pro Ser Phe Tyr
    930   935   940

His Leu Ser Glu Ile Val Glu Asn Leu Leu Pro Gly Gln Tyr Lys Lys
945   950   955   960

Ser Tyr Glu Lys Ile His Leu Asp Phe Leu Lys Ser Asp His Pro Ala
            965   970   975

Val Ala Arg Met Arg Val Asp Ser Asp Asn Ala Tyr Ile Gly Val Thr
            980   985   990

Tyr Lys Asn Glu Glu Asp Lys Leu Lys Asp Trp Glu Gly Gly Leu Asp
        995   1000   1005

Glu Gln Arg Leu Ser Ala Asp Ser Gly Tyr Ile Ile Pro Leu Pro Asp
    1010   1015   1020

Ile Asp Pro Val Pro Glu Glu Glu Asp Leu Gly Lys Arg Asn Arg His
1025   1030   1035   1040

Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser Ser Ser
            1045   1050   1055

Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile Asp Met
            1060   1065   1070

Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp Ser Phe
        1075   1080   1085

Leu   *
1090

(2) INFORMATION FOR SEQ ID NO:3:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 5427 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
    (A) NAME/KEY: CDS
    (B) LOCATION: 187..3507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
TGTTCTCCTG AGCCTTCAGG AGCCTGCACC AGTCCTGCCT GTCCTTCTAC TCAGCTGTTA        60

CCCACTCTGG GACCAGCAGT CTTTCTGATA ACTGGGAGAG GGCAGTAAGG AGGACTTCCT       120

GGAGGGGGTG ACTGTCCAGA GCCTGGAACT GTGCCCACAC CAGAAGCCAT CAGCAGCAAG       180

GACACC ATG CGG CTT CCG GGT GCG ATG CCA GCT CTG GCC CTC AAA GGC         228
       Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly
             1095                    1100

GAG CTG CTG TTG CTG TCT CTC CTG TTA CTT CTG GAA CCA CAG ATC TCT        276
Glu Leu Leu Leu Leu Ser Leu Leu Leu Leu Leu Glu Pro Gln Ile Ser
1105                1110                1115                1120

CAG GGC CTG GTC GTC ACA CCC CCG GGG CCA GAG CTT GTC CTC AAT GTC        324
Gln Gly Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val
                1125                1130                1135

TCC AGC ACC TTC GTT CTG ACC TGC TCG GGT TCA GCT CCG GTG GTG TGG        372
Ser Ser Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp
                1140                1145                1150

GAA CGG ATG TCC CAG GAG CCC CCA CAG GAA ATG GCC AAG GCC CAG GAT        420
Glu Arg Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp
            1155                1160                1165

GGC ACC TTC TCC AGC GTG CTC ACA CTG ACC AAC CTC ACT GGG CTA GAC        468
Gly Thr Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp
    1170                1175                1180

ACG GGA GAA TAC TTT TGC ACC CAC AAT GAC TCC CGT GGA CTG GAG ACC        516
Thr Gly Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr
1185                1190                1195                1200

GAT GAG CGG AAA CGG CTC TAC ATC TTT GTG CCA GAT CCC ACC GTG GGC        564
Asp Glu Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly
                1205                1210                1215

TTC CTC CCT AAT GAT GCC GAG GAA CTA TTC ATC TTT CTC ACG GAA ATA        612
Phe Leu Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile
                1220                1225                1230

ACT GAG ATC ACC ATT CCA TGC CGA GTA ACA GAC CCA CAG CTG GTG GTG        660
Thr Glu Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val
                1235                1240                1245

ACA CTG CAC GAG AAG AAA GGG GAC GTT GCA CTG CCT GTC CCC TAT GAT        708
Thr Leu His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp
    1250                1255                1260

CAC CAA CGT GGC TTT TCT GGT ATC TTT GAG GAC AGA AGC TAC ATC TGC        756
His Gln Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys
1265                1270                1275                1280

AAA ACC ACC ATT GGG GAC AGG GAG GTG GAT TCT GAT GCC TAC TAT GTC        804
Lys Thr Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val
                1285                1290                1295
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TAC AGA CTC CAG GTG TCA TCC ATC AAC GTC TCT GTG AAC GCA GTG CAG        852
Tyr Arg Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln
            1300                1305                1310

ACT GTG GTC CGC CAG GGT GAG AAC ATC ACC CTC ATG TGC ATT GTG ATC        900
Thr Val Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile
            1315                1320                1325

GGG AAT GAT GTG GTC AAC TTC GAG TGG ACA TAC CCC CGC AAA GAA AGT        948
Gly Asn Asp Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser
        1330                1335                1340

GGG CGG CTG GTG GAG CCG GTG ACT GAC TTC CTC TTG GAT ATG CCT TAC        996
Gly Arg Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr
1345                1350                1355                1360

CAC ATC CGC TCC ATC CTG CAC ATC CCC AGT GCC GAG TTA GAA GAC TCG       1044
His Ile Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser
            1365                1370                1375

GGG ACC TAC ACC TGC AAT GTG ACG GAG AGT GTG AAT GAC CAT CAG GAT       1092
Gly Thr Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp
            1380                1385                1390

GAA AAG GCC ATC AAC ATC ACC GTG GTT GAG AGC GGC TAC GTG CGG CTC       1140
Glu Lys Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu
        1395                1400                1405

CTG GGA GAG GTG GGC ACA CTA CAA TTT GCT GAG CTG CAT CGG AGC CGG       1188
Leu Gly Glu Val Gly Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg
        1410                1415                1420

ACA CTG CAG GTA GTG TTC GAG GCC TAC CCA CCG CCC ACT GTC CTG TGG       1236
Thr Leu Gln Val Val Phe Glu Ala Tyr Pro Pro Pro Thr Val Leu Trp
1425                1430                1435                1440

TTC AAA GAC AAC CGC ACC CTG GGC GAC TCC AGC GCT GGC GAA ATC GCC       1284
Phe Lys Asp Asn Arg Thr Leu Gly Asp Ser Ser Ala Gly Glu Ile Ala
            1445                1450                1455

CTG TCC ACG CGC AAC GTG TCG GAG ACC CGG TAT GTG TCA GAG CTG ACA       1332
Leu Ser Thr Arg Asn Val Ser Glu Thr Arg Tyr Val Ser Glu Leu Thr
            1460                1465                1470

CTG GTT CGC GTG AAG GTG GCA GAG GCT GGC CAC TAC ACC ATG CGG GCC       1380
Leu Val Arg Val Lys Val Ala Glu Ala Gly His Tyr Thr Met Arg Ala
            1475                1480                1485

TTC CAT GAG GAT GCT GAG GTC CAG CTC TCC TTC CAG CTA CAG ATC AAT       1428
Phe His Glu Asp Ala Glu Val Gln Leu Ser Phe Gln Leu Gln Ile Asn
        1490                1495                1500

GTC CCT GTC CGA GTG CTG GAG CTA AGT GAG AGC CAC CCT GAC AGT GGG       1476
Val Pro Val Arg Val Leu Glu Leu Ser Glu Ser His Pro Asp Ser Gly
1505                1510                1515                1520

GAA CAG ACA GTC CGC TGT CGT GGC CGG GGC ATG CCG CAG CCG AAC ATC       1524
Glu Gln Thr Val Arg Cys Arg Gly Arg Gly Met Pro Gln Pro Asn Ile
            1525                1530                1535

ATC TGG TCT GCC TGC AGA GAC CTC AAA AGG TGT CCA CGT GAG CTG CCG       1572
Ile Trp Ser Ala Cys Arg Asp Leu Lys Arg Cys Pro Arg Glu Leu Pro
            1540                1545                1550

CCC ACG CTG CTG GGG AAC AGT TCC GAA GAG GAG AGC CAG CTG GAG ACT       1620
Pro Thr Leu Leu Gly Asn Ser Ser Glu Glu Glu Ser Gln Leu Glu Thr
            1555                1560                1565
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TAT GTG CCC ATG CTG GAC ATG AAA GGA GAC GTC AAA TAT GCA GAC ATC          2484
Tyr Val Pro Met Leu Asp Met Lys Gly Asp Val Lys Tyr Ala Asp Ile
            1845            1850            1855

GAG TCC TCC AAC TAC ATG GCC CCT TAC GAT AAC TAC GTT CCC TCT GCC          2532
Glu Ser Ser Asn Tyr Met Ala Pro Tyr Asp Asn Tyr Val Pro Ser Ala
            1860            1865            1870

CCT GAG AGG ACC TGC CGA GCA ACT TTG ATC AAC GAG TCT CCA GTG CTA          2580
Pro Glu Arg Thr Cys Arg Ala Thr Leu Ile Asn Glu Ser Pro Val Leu
            1875            1880            1885

AGC TAC ATG GAC CTC GTG GGC TTC AGC TAC CAG GTG GCC AAT GGC ATG          2628
Ser Tyr Met Asp Leu Val Gly Phe Ser Tyr Gln Val Ala Asn Gly Met
            1890            1895            1900

GAG TTT CTG GCC TCC AAG AAC TGC GTC CAC AGA GAC CTG GCG GCT AGG          2676
Glu Phe Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg
1905            1910            1915            1920

AAC GTG CTC ATC TGT GAA GGC AAG CTG GTC AAG ATC TGT GAC TTT GGC          2724
Asn Val Leu Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly
            1925            1930            1935

CTG GCT CGA GAC ATC ATG CGG GAC TCG AAT TAC ATC TCC AAA GGC AGC          2772
Leu Ala Arg Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser
            1940            1945            1950

ACC TTT TTG CCT TTA AAG TGG ATG GCT CCG GAG AGC ATC TTC AAC AGC          2820
Thr Phe Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser
            1955            1960            1965

CTC TAC ACC ACC CTG AGC GAC GTG TGG TCC TTC GGG ATC CTG CTC TGG          2868
Leu Tyr Thr Thr Leu Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp
            1970            1975            1980

GAG ATC TTC ACC TTG GGT GGC ACC CCT TAC CCA GAG CTG CCC ATG AAC          2916
Glu Ile Phe Thr Leu Gly Gly Thr Pro Tyr Pro Glu Leu Pro Met Asn
1985            1990            1995            2000

GAG CAG TTC TAC AAT GCC ATC AAA CGG GGT TAC CGC ATG GCC CAG CCT          2964
Glu Gln Phe Tyr Asn Ala Ile Lys Arg Gly Tyr Arg Met Ala Gln Pro
            2005            2010            2015

GCC CAT GCC TCC GAC GAG ATC TAT GAG ATC ATG CAG AAG TGC TGG GAA          3012
Ala His Ala Ser Asp Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu
            2020            2025            2030

GAG AAG TTT GAG ATT CGG CCC CCC TTC TCC CAG CTG GTG CTG CTT CTC          3060
Glu Lys Phe Glu Ile Arg Pro Pro Phe Ser Gln Leu Val Leu Leu Leu
            2035            2040            2045

GAG AGA CTG TTG GGC GAA GGT TAC AAA AAG AAG TAC CAG CAG GTG GAT          3108
Glu Arg Leu Leu Gly Glu Gly Tyr Lys Lys Lys Tyr Gln Gln Val Asp
            2050            2055            2060

GAG GAG TTT CTG AGG AGT GAC CAC CCA GCC ATC CTT CGG TCC CAG GCC          3156
Glu Glu Phe Leu Arg Ser Asp His Pro Ala Ile Leu Arg Ser Gln Ala
2065            2070            2075            2080

CGC TTG CCT GGG TTC CAT GGC CTC CGA TCT CCC CTG GAC ACC AGC TCC          3204
Arg Leu Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser Ser
            2085            2090            2095

GTC CTC TAT ACT GCC GTG CAG CCC AAT GAG GGT GAC AAC GAC TAT ATC          3252
Val Leu Tyr Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp Tyr Ile
            2100            2105            2110
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```
GGTCTGCGTC GAAGACAGAA TGGACAGTGA GGACAGTTAT GTCTTGTAAA AGACAAGAAG    4927

CTTCAGATGG GTACCCCAAG AAGGATGTGA GAGGTGGGCG CTTTGGAGGT TTGCCCCTCA    4987

CCCACCAGCT GCCCCATCCC TGAGGCAGCG CTCCATGGGG GTATGGTTTT GTCACTGCCC    5047

AGACCTAGCA GTGACATCTC ATTGTCCCCA GCCCAGTGGG CATTGGAGGT GCCAGGGGAG    5107

TCAGGGTTGT AGCCAAGACG CCCCCGCACG GGGAGGGTTG GGAAGGGGGT GCAGGAAGCT    5167

CAACCCCTCT GGGCACCAAC CCTGCATTGC AGGTTGGCAC CTTACTTCCC TGGGATCCCA    5227

GAGTTGGTCC AAGGAGGGAG AGTGGGTTCT CAATACGGTA CCAAAGATAT AATCACCTAG    5287

GTTTACAAAT ATTTTTAGGA CTCACGTTAA CTCACATTTA TACAGCAGAA ATGCTATTTT    5347

GTATGCTGTT AAGTTTTTCT ATCTGTGTAC TTTTTTTTAA GGGAAAGATT TTAATATTAA    5407

ACCTGGTGCT TCTCACTCAC                                                5427
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1107 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly Glu Leu
 1               5              10              15

Leu Leu Leu Ser Leu Leu Leu Leu Leu Glu Pro Gln Ile Ser Gln Gly
            20              25              30

Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val Ser Ser
            35              40              45

Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp Glu Arg
        50              55              60

Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp Gly Thr
 65              70              75              80

Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp Thr Gly
                85              90              95

Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr Asp Glu
            100             105             110

Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly Phe Leu
        115             120             125

Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile Thr Glu
        130             135             140

Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val Thr Leu
145             150             155             160

His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp His Gln
                165             170             175

Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys Lys Thr
            180             185             190
```

Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val Tyr Arg
        195   200   205

Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln Thr Val
    210   215   220

Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile Gly Asn
225   230   235   240

Asp Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser Gly Arg
            245   250   255

Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr His Ile
            260   265   270

Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser Gly Thr
        275   280   285

Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp Glu Lys
    290   295   300

Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu Leu Gly
305   310   315   320

Glu Val Gly Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg Thr Leu
            325   330   335

Gln Val Val Phe Glu Ala Tyr Pro Pro Thr Val Leu Trp Phe Lys
            340   345   350

Asp Asn Arg Thr Leu Gly Asp Ser Ser Ala Gly Glu Ile Ala Leu Ser
        355   360   365

Thr Arg Asn Val Ser Glu Thr Arg Tyr Val Ser Glu Leu Thr Leu Val
    370   375   380

Arg Val Lys Val Ala Glu Ala Gly His Tyr Thr Met Arg Ala Phe His
385   390   395   400

Glu Asp Ala Glu Val Gln Leu Ser Phe Gln Leu Gln Ile Asn Val Pro
            405   410   415

Val Arg Val Leu Glu Leu Ser Glu Ser His Pro Asp Ser Gly Glu Gln
            420   425   430

Thr Val Arg Cys Arg Gly Arg Gly Met Pro Gln Pro Asn Ile Ile Trp
        435   440   445

Ser Ala Cys Arg Asp Leu Lys Arg Cys Pro Arg Glu Leu Pro Pro Thr
    450   455   460

Leu Leu Gly Asn Ser Ser Glu Glu Glu Ser Gln Leu Glu Thr Asn Val
465   470   475   480

Thr Tyr Trp Glu Glu Glu Gln Glu Phe Glu Val Val Ser Thr Leu Arg
            485   490   495

Leu Gln His Val Asp Arg Pro Leu Ser Val Arg Cys Thr Leu Arg Asn
            500   505   510

Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu
            515   520   525

Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu
    530   535   540

Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro
545   550   555   560

Arg Tyr Glu Il Arg Trp Lys Val Ile Glu Ser Val Ser Ser Asp Gly
                565   570   575

His Glu Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp Ser Thr
            580   585   590

Trp Glu Leu Pro Arg Asp Gln Leu Val Leu Gly Arg Thr Leu Gly Ser
        595   600   605

Gly Ala Phe Gly Gln Val Val Glu Ala Thr Ala His Gly Leu Ser His
    610   615   620

Ser Gln Ala Thr Met Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala
625   630   635   640

Arg Ser Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys Ile Met Ser
            645   650   655

His Leu Gly Pro His Leu Asn Val Val Asn Leu Leu Gly Ala Cys Thr
            660   665   670

Lys Gly Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Arg Tyr Gly Asp
        675   680   685

Leu Val Asp Tyr Leu His Arg Asn Lys His Thr Phe Leu Gln His His
    690   695   700

Ser Asp Lys Arg Arg Pro Pro Ser Ala Glu Leu Tyr Ser Asn Ala Leu
705   710   715   720

Pro Val Gly Leu Pro Leu Pro Ser His Val Ser Leu Thr Gly Glu Ser
            725   730   735

Asp Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Val Asp Tyr Val
            740   745   750

Pro Met Leu Asp Met Lys Gly Asp Val Lys Tyr Ala Asp Ile Glu Ser
        755   760   765

Ser Asn Tyr Met Ala Pro Tyr Asp Asn Tyr Val Pro Ser Ala Pro Glu
    770   775   780

Arg Thr Cys Arg Ala Thr Leu Ile Asn Glu Ser Pro Val Leu Ser Tyr
785   790   795   800

Met Asp Leu Val Gly Phe Ser Tyr Gln Val Ala Asn Gly Met Glu Phe
            805   810   815

Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn Val
            820   825   830

Leu Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly Leu Ala
        835   840   845

Arg Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser Thr Phe
    850   855   860

Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser Leu Tyr
865   870   875   880

Thr Thr Leu Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile
            885   890   895

```
Phe Thr Leu Gly Gly Thr Pro Tyr Pro Glu Leu Pro Met Asn Glu Gln
            900             905             910

Phe Tyr Asn Ala Ile Lys Arg Gly Tyr Arg Met Ala Gln Pro Ala His
            915             920             925

Ala Ser Asp Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu Glu Lys
    930             935             940

Phe Glu Ile Arg Pro Pro Phe Ser Gln Leu Val Leu Leu Leu Glu Arg
945             950             955             960

Leu Leu Gly Glu Gly Tyr Lys Lys Lys Tyr Gln Gln Val Asp Glu Glu
            965             970             975

Phe Leu Arg Ser Asp His Pro Ala Ile Leu Arg Ser Gln Ala Arg Leu
            980             985             990

Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser Ser Val Leu
            995             1000            1005

Tyr Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp Tyr Ile Ile Pro
    1010            1015            1020

Leu Pro Asp Pro Lys Pro Glu Val Ala Asp Glu Gly Pro Leu Glu Gly
1025            1030            1035            1040

Ser Pro Ser Leu Ala Ser Ser Thr Leu Asn Glu Val Asn Thr Ser Ser
            1045            1050            1055

Thr Ile Ser Cys Asp Ser Pro Leu Glu Pro Gln Asp Glu Pro Glu Pro
            1060            1065            1070

Glu Pro Gln Leu Glu Leu Gln Val Glu Pro Glu Pro Glu Leu Glu Gln
            1075            1080            1085

Leu Pro Asp Ser Gly Cys Pro Ala Pro Arg Ala Glu Ala Glu Asp Ser
            1090            1095            1100

Phe Leu  *
1105
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:
        (A) NAME/KEY: Peptide
        (B) LOCATION: 1..20
        (D) OTHER INFORMATION: /note= "Peptide Y719"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro
1               5               10              15

Met Leu Asp Met
            20
```

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:
        (A) NAME/KEY: Peptide
        (B) LOCATION: 1..20
        (D) OTHER INFORMATION: /note= "Peptide Y719P. Contains a
phosphate group at position 14."

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro
1   5   10   15

Met Leu Asp Met
        20

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:
        (A) NAME/KEY: Peptide
        (B) LOCATION: 1..20
        (D) OTHER INFORMATION: /note= "Peptide Y708P. Contains a
phosphate group at position 3."

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro
1   5   10   15

Met Leu Asp Met
        20

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:
        (A) NAME/KEY: Peptide
        (B) LOCATION: 1..17
        (D) OTHER INFORMATION: /note= "Peptide Y719P short.

Contains a phosphate gr up at position 11."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro Met Leu Asp
1   5   10   15

Met

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:
        (A) NAME/KEY: Peptide
        (B) LOCATION: 1..13
        (D) OTHER INFORMATION: /note= "Peptide Y708P short.
Contains a phosphate group at position 3."

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp
1   5   10

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:
        (A) NAME/KEY: Peptide
        (B) LOCATION: 1..20
        (D) OTHER INFORMATION: /note= "Peptide Y708P/F719.
Contains a phosphate group at position 3."

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Phe Val Pro
1   5   10   15

Met Leu Asp Met
                20

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

```
        Asp Leu Gly Gly
                 20
```

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: DNA

   (ix) FEATURES:
        (D) OTHER INFORMATION: /note= "N is A, C, G, or T"

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTSCGNGCN GCCAGNTCSC GNTG   24